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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/973,424A

DATE: 05/09/2002

TIME: 12:54:04

Input Set : A:\cura85cip.txt

Output Set: N:\CRF3\05092002\I973424A.raw

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3 <110> APPLICANT: Prayaga, Sudhirdas K
4     Taupier Jr, Raymond J
5     Bandaru, Raj
7 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDES HOMOLOGOUS TO THYMOSIN, EPHRIN A
8     RECEPTORS, AND FIBROMODULIN, AND POLYNUCLEOTIDES
9     ENCODING SAME
11 <130> FILE REFERENCE: 15966-585 CIP2
13 <140> CURRENT APPLICATION NUMBER: 09/973,424A
14 <141> CURRENT FILING DATE: 2001-10-09
16 <150> PRIOR APPLICATION NUMBER: 60/159,805
17 <151> PRIOR FILING DATE: 1999-10-15
19 <150> PRIOR APPLICATION NUMBER: 60/159,992
20 <151> PRIOR FILING DATE: 1999-10-18
22 <150> PRIOR APPLICATION NUMBER: 60/160,952
23 <151> PRIOR FILING DATE: 1999-10-22
25 <150> PRIOR APPLICATION NUMBER: 09/689,486
26 <151> PRIOR FILING DATE: 2000-10-12
28 <150> PRIOR APPLICATION NUMBER: 09/687,276
29 <151> PRIOR FILING DATE: 2000-10-13
31 <160> NUMBER OF SEQ ID NOS: 84
33 <170> SOFTWARE: PatentIn Ver. 2.1
35 <210> SEQ ID NO: 1
36 <211> LENGTH: 430
37 <212> TYPE: DNA
38 <213> ORGANISM: Homo sapiens
40 <220> FEATURE:
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42 <222> LOCATION: (61)..(234)
44 <400> SEQUENCE: 1
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47 atg gca gac aaa cca gac ata ggg gaa atc gcc agc ttc aat aag gcc 108
48 Met Ala Asp Lys Pro Asp Ile Gly Glu Ile Ala Ser Phe Asn Lys Ala
49 1 5 10 15
51 aag ctg aag aaa aca gag atg cag gag aac acc ctg ctg acc aaa gag 156
52 Lys Leu Lys Lys Thr Glu Met Gln Glu Asn Thr Leu Leu Thr Lys Glu
53 20 25 30
55 gcc att gag cag gag aag cgg gtg aaa ttt cct aag agc ctg gag gat 204
56 Ala Ile Glu Gln Glu Lys Arg Val Lys Phe Pro Lys Ser Leu Glu Asp
57 35 40 45
59 tcc cta ccc ctg tca tct tct aga ccc cag tagtaatgtg gaggaagaat 254
60 Ser Leu Pro Leu Ser Ser Ser Arg Pro Gln
61 50 55
63 caccacaaga tggacacaag ccacaaactg tgacgtgaac ctgggcactc cgtgctgatg 314

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65 ccaccagcct gaggggtccct atgggtccaa tcagactgcc aaattctctg gtttgccctg 374
67 ggatattata gaaaattatt tgcgtgaata atgaaaacac agtcatggc aaaaaa 430
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79 Lys Leu Lys Lys Thr Glu Met Gln Glu Asn Thr Leu Leu Thr Lys Glu
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82 Ala Ile Glu Gln Glu Lys Arg Val Lys Phe Pro Lys Ser Leu Glu Asp
83 35 40 45
85 Ser Leu Pro Leu Ser Ser Ser Arg Pro Gln
86 50 55
90 <210> SEQ ID NO: 3
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108 cacgggggact ggggctggct caggtatccg gctcatgggt gggactccat caacgaggtg 180
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113 cagttcctca aaatcgacac cattgcggcc gacgagagct tcacaggtgc cgaccttgg 480
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124 acctacaatg ccgtgtgccg ccgtgccccc tgggcactga gccgtgcga ggcatgtggg 1140
125 agcggcaccc gctttgtgcc ccagcagaca agcctggtgc aggcagcct gctgggtggc 1200
126 aacctgctgg ccacatgaa ctactccttc tggatcgagg ccgtcaatgg cgtgtccgac 1260
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130 gacaaggaga tgcagagcta ctocaccctc aaggccgtca ccaccagagc caccgtctcc 1500
131 ggcctcaagc cgggcacccg ctacgtgttc caggctccgag ccgcacacctc agcaggctgt 1560
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133 aggaccattg tctggtctg cctgacgctc atcacgggccc tgggtgtgct tctgctcctg 1680
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135 aagatgcaact atcagaatgg acaggcacc ccacctgtct tccgtgctct gcatcaccct 1800
136 ccgggaaagc tcccagagcc ccagttctat gcggaacccc acacctacga ggagccaggc 1860
137 cgggcgggcc gcagtttcac tcgggagatc gaggcctcta ggatccacat cgagaaaatc 1920
138 atcggtctcg gagactccgg ggaagtctgc tacgggaggc tgcgggtgcc agggcagcgg 1980
139 gatgtgcccc tggccatcaa ggcctcaaa gccggctaca cggagagaca gaggcgggac 2040
140 ttcctgagcg aggcgtccat catggggcaa ttcgaccatc ccaacatcat ccgctcagag 2100
141 ggtgtcgtca cccgtggccg cctggcaatg attgtgactg agtacatgga gaacggctct 2160
142 ctggacacct tcctgaggac ccacgacggg cagttcacca tcatgcagct ggtgggcatg 2220
143 ctgagaggag tgggtgccgg catgagctac ctctcagacc tgggctatgt ccaccgagac 2280
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147 gtgtggagct tcggcgtggt catgtgggag gtgctggcct atggggagcg gccctactgg 2520
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161 <212> TYPE: PRT
162 <213> ORGANISM: Homo sapiens
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169 20 25 30
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172 35 40 45
174 Tyr Pro Ala His Gly Trp Asp Ser Ile Asn Glu Val Asp Glu Ser Phe
175 50 55 60
177 Gln Pro Ile His Thr Tyr Gln Val Cys Asn Val Met Ser Pro Asn Gln
178 65 70 75 80
180 Asn Asn Trp Leu Arg Thr Ser Trp Val Pro Arg Asp Gly Ala Arg Arg
181 85 90 95
183 Val Tyr Ala Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Met Pro
184 100 105 110
186 Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Leu Glu

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190		130				135					140			
192	Ile	Asp	Thr	Ile	Ala	Ala	Asp	Glu	Ser	Phe	Thr	Gly	Ala	Asp
193	145				150						155			160
195	Val	Arg	Arg	Leu	Lys	Leu	Asn	Thr	Glu	Val	Arg	Ser	Val	Gly
196				165					170					175
198	Ser	Lys	Arg	Gly	Phe	Tyr	Leu	Ala	Phe	Gln	Asp	Ile	Gly	Ala
199			180					185					190	
201	Ala	Ile	Leu	Ser	Leu	Arg	Ile	Tyr	Tyr	Lys	Lys	Cys	Pro	Ala
202		195					200					205		
204	Arg	Asn	Leu	Ala	Ala	Phe	Ser	Glu	Ala	Val	Thr	Gly	Ala	Asp
205		210				215					220			
207	Ser	Leu	Val	Glu	Val	Arg	Gly	Gln	Cys	Val	Arg	His	Ser	Glu
208	225			230						235				240
210	Asp	Thr	Pro	Lys	Met	Tyr	Cys	Ser	Ala	Glu	Gly	Glu	Trp	Leu
211				245					250					255
213	Ile	Gly	Lys	Cys	Val	Cys	Ser	Ala	Gly	Tyr	Glu	Glu	Arg	Arg
214			260					265					270	
216	Cys	Val	Ala	Cys	Glu	Leu	Gly	Phe	Tyr	Lys	Ser	Ala	Pro	Gly
217		275					280					285		
219	Leu	Cys	Ala	Arg	Cys	Pro	Pro	His	Ser	His	Ser	Ala	Ala	Pro
220		290				295					300			
222	Gln	Ala	Cys	His	Cys	Asp	Leu	Ser	Tyr	Tyr	Arg	Ala	Ala	Leu
223	305			310						315				320
225	Pro	Ser	Ser	Ala	Cys	Thr	Arg	Pro	Pro	Ser	Ala	Pro	Val	Asn
226				325					330					335
228	Ser	Ser	Val	Asn	Gly	Thr	Ser	Val	Thr	Leu	Glu	Trp	Ala	Pro
229			340					345					350	
231	Asp	Pro	Gly	Gly	Arg	Ser	Asp	Ile	Thr	Tyr	Asn	Ala	Val	Cys
232		355					360					365		
234	Cys	Pro	Trp	Ala	Leu	Ser	Arg	Cys	Glu	Ala	Cys	Gly	Ser	Gly
235		370				375					380			
237	Phe	Val	Pro	Gln	Gln	Thr	Ser	Leu	Val	Gln	Ala	Ser	Leu	Leu
238	385				390					395				400
240	Asn	Leu	Leu	Ala	His	Met	Asn	Tyr	Ser	Phe	Trp	Ile	Glu	Ala
241				405					410					415
243	Gly	Val	Ser	Asp	Leu	Ser	Pro	Glu	Pro	Arg	Arg	Ala	Ala	Val
244			420					425					430	
246	Ile	Thr	Thr	Asn	Gln	Ala	Ala	Pro	Ser	Gln	Val	Val	Val	Ile
247		435					440					445		
249	Glu	Arg	Ala	Gly	Gln	Thr	Ser	Val	Ser	Leu	Leu	Trp	Gln	Glu
250		450				455					460			
252	Gln	Pro	Asn	Gly	Ile	Ile	Leu	Glu	Tyr	Glu	Ile	Lys	Tyr	Tyr
253	465				470					475				480
255	Asp	Lys	Glu	Met	Gln	Ser	Tyr	Ser	Thr	Leu	Lys	Ala	Val	Thr
256				485					490					495
258	Ala	Thr	Val	Ser	Gly	Leu	Lys	Pro	Gly	Thr	Arg	Tyr	Val	Phe
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264 Val Glu Thr Gly Lys Pro Arg Pro Arg Tyr Asp Thr Arg Thr Ile Val
265      530      535      540
267 Trp Ile Cys Leu Thr Leu Ile Thr Gly Leu Val Val Leu Leu Leu Leu
268 545      550      555      560
270 Leu Ile Cys Lys Lys Arg His Cys Gly Tyr Ser Lys Ala Phe Gln Asp
271      565      570      575
273 Ser Asp Glu Glu Lys Met His Tyr Gln Asn Gly Gln Ala Pro Pro Pro
274      580      585      590
276 Val Phe Leu Pro Leu His His Pro Pro Gly Lys Leu Pro Glu Pro Gln
277      595      600      605
279 Phe Tyr Ala Glu Pro His Thr Tyr Glu Glu Pro Gly Arg Ala Gly Arg
280      610      615      620
282 Ser Phe Thr Arg Glu Ile Glu Ala Ser Arg Ile His Ile Glu Lys Ile
283 625      630      635      640
285 Ile Gly Ser Gly Asp Ser Gly Glu Val Cys Tyr Gly Arg Leu Arg Val
286      645      650      655
288 Pro Gly Gln Arg Asp Val Pro Val Ala Ile Lys Ala Leu Lys Ala Gly
289      660      665      670
291 Tyr Thr Glu Arg Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met
292      675      680      685
294 Gly Gln Phe Asp His Pro Asn Ile Ile Arg Leu Glu Gly Val Val Thr
295      690      695      700
297 Arg Gly Arg Leu Ala Met Ile Val Thr Glu Tyr Met Glu Asn Gly Ser
298 705      710      715      720
300 Leu Asp Thr Phe Leu Arg Thr His Asp Gly Gln Phe Thr Ile Met Gln
301      725      730      735
303 Leu Val Gly Met Leu Arg Gly Val Gly Ala Gly Met Arg Tyr Leu Ser
304      740      745      750
306 Asp Leu Gly Tyr Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val
307      755      760      765
309 Asp Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val
310      770      775      780
312 Leu Glu Asp Asp Pro Asp Ala Ala Tyr Thr Thr Thr Gly Gly Lys Ile
313 785      790      795      800
315 Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Phe Arg Thr Phe Ser
316      805      810      815
318 Ser Ala Ser Asp Val Trp Ser Phe Gly Val Val Met Trp Glu Val Leu
319      820      825      830
321 Ala Tyr Gly Glu Arg Pro Tyr Trp Asn Met Thr Asn Arg Asp Val Ile
322      835      840      845
324 Ser Ser Val Glu Glu Gly Tyr Arg Leu Pro Ala Pro Met Gly Cys Pro
325      850      855      860
327 His Ala Leu His Gln Leu Met Leu Asp Cys Trp His Lys Asp Arg Ala
328 865      870      875      880
330 Gln Arg Pro Arg Phe Ser Gln Ile Val Ser Val Leu Asp Ala Leu Ile
331      885      890      895
333 Arg Ser Pro Glu Ser Leu Arg Ala Thr Ala Thr Val Ser Arg Cys Pro

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VERIFICATION SUMMARY

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